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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 23:34:14 ; Search time 127 Seconds
(without alignments)
257.681 Million cell updates/sec

Title: US-10-797-822-1

Perfect score: 20

Sequence: 1 atgatggcggcgagtgatgca 20

Scoring table: 
Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	442	US-09-621-976-13204	Sequence 13204, A
2	20	100.0	467	US-09-513-999C-1128	Sequence 1128, Ap
3	20	100.0	2518	US-09-433-699-3	Sequence 3, Appl
4	20	100.0	2527	US-09-949-016-4169	Sequence 4169, Ap
5	20	100.0	13489	US-09-949-016-15911	Sequence 15911, A
6	18	90.0	20	US-09-433-699-14	Sequence 14, Appl
7	15	75.0	597	US-09-134-000C-2181	Sequence 2181, Ap
8	15	75.0	1176	US-09-489-039A-2620	Sequence 2620, Ap
9	15	75.0	1211	US-09-270-767-31566	Sequence 31566, A
10	15	75.0	1295	US-09-489-039A-2450	Sequence 2450, Ap
11	15	75.0	1498	US-09-270-767-15231	Sequence 15231, A
12	15	75.0	2118	US-09-902-540-3960	Sequence 3960, Ap
13	15	75.0	18324	US-09-902-540-1196	Sequence 1196, Ap
14	15	75.0	160018	US-09-949-016-12617	Sequence 12617, A
15	15	75.0	160018	US-09-949-016-15994	Sequence 15994, A
16	14	70.0	392	US-09-702-705-1570	Sequence 1570, Ap
17	14	70.0	392	US-09-736-457-1570	Sequence 1570, Ap
18	14	70.0	392	US-09-614-124B-1570	Sequence 1570, Ap
19	14	70.0	392	US-09-671-325-1570	Sequence 1570, Ap
20	14	70.0	392	US-09-658-824-1570	Sequence 1570, Ap
21	14	70.0	819	US-08-998-416-336	Sequence 336, App
22	14	70.0	1057	US-09-452-239-5	Sequence 5, Appl
23	14	70.0	1229	US-08-790-572-2	Sequence 2, Appl
24	14	70.0	1229	US-09-213-396-2	Sequence 2, Appl
25	14	70.0	1230	US-09-016-434-585	Sequence 585, App
26	14	70.0	1336	US-09-180-109A-28	Sequence 28, Appl
27	14	70.0	1420	US-09-180-109A-23	Sequence 23, Appl

c	28	14	70.0	1452	4	US-09-252-991A-4444	Sequence 4444, Ap
c	29	14	70.0	1671	4	US-09-252-991A-4648	Sequence 4648, Ap
c	30	14	70.0	1680	4	US-09-902-540-8972	Sequence 8972, Ap
c	31	14	70.0	2115	4	US-09-252-991A-4163	Sequence 4163, Ap
c	32	14	70.0	2166	4	US-09-902-540-8129	Sequence 8129, Ap
c	33	14	70.0	2343	4	US-09-976-594-986	Sequence 986, App
c	34	14	70.0	2529	4	US-09-815-923-15	Sequence 15, Appl
c	35	14	70.0	2690	4	US-08-524-757-11	Sequence 11, Appl
c	36	14	70.0	2885	4	US-09-016-434-1143	Sequence 1143, Ap
c	37	14	70.0	3501	1	US-08-524-757-5	Sequence 5, Appl
c	38	14	70.0	3802	1	US-08-404-354B-2	Sequence 2, Appl
c	39	14	70.0	3802	1	US-08-314-083B-2	Sequence 2, Appl
c	40	14	70.0	3802	1	US-08-435-675B-2	Sequence 2, Appl
c	41	14	70.0	3802	1	US-08-336-257A-4	Sequence 4, Appl
c	42	14	70.0	3802	3	US-08-884-599-2	Sequence 2, Appl
c	43	14	70.0	3802	6	5386025-7	Sequence 2, Appl
c	44	14	70.0	3802	6	5386025-7	Sequence 2, Appl
c	45	14	70.0	5499	4	US-09-902-540-2892	Sequence 2892, Ap

ALIGNMENTS

RESULT 1
US-09-621-976-13204/C
Sequence 13204, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Malne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 13204
LENGTH: 442
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-13204

Query Match 100.0%; Score 20; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGCA 20
|||||
Db 166 ATGATGGCGCGGAGTGCA 147
|||||

RESULT 2
US-09-513-999C-1128/C
Sequence 1128, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Malne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 1128
LENGTH: 467
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS
LOCATION: 162..467
US-09-513-999C-1128

Query Match 100.0%; Score 20; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20
DB 163 ATGATGCGCGCGAGTGTGA 144

RESULT 3
US-09-433-699-3/c
Sequence 3, Application US/09433699B
Patent No. 6165786
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
FILE REFERENCE: RTS-0109
CURRENT APPLICATION NUMBER: US/09/433,699B
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
LENGTH: 2518
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (112)..(2235)
US-09-433-699-3

Query Match 100.0%; Score 20; DB 3; Length 2518;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20
DB 113 ATGATGCGCGCGAGTGTGA 94

RESULT 4
US-09-949-016-4169/c
Sequence 4169, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4169
LENGTH: 2527
TYPE: DNA
ORGANISM: Human
US-09-949-016-4169

Query Match 100.0%; Score 20; DB 4; Length 2527;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20
DB 113 ATGATGCGCGCGAGTGTGA 94

RESULT 5
US-09-949-016-15911/c
Sequence 15911, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15911
LENGTH: 13489
TYPE: DNA
ORGANISM: Human
US-09-949-016-15911

Query Match 100.0%; Score 20; DB 4; Length 13489;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20
DB 2113 ATGATGCGCGCGAGTGTGA 2094

RESULT 6
US-09-433-699-14
Sequence 14, Application US/09433699B
Patent No. 6165786
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
FILE REFERENCE: RTS-0109
CURRENT APPLICATION NUMBER: US/09/433,699B
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 14
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-433-699-14

Query Match 90.0%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGT 18
DB 3 ATGATGCGCGCGAGTGT 20

RESULT 7
US-09-134-000C-2181
Sequence 2181, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:

```

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2181
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2181

Query Match          75.0%; Score 15; DB 4; Length 597;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GATGCGCGCGAGTG 17
        |||||||
        496 GATGCGCGCGAGTG 510

RESULT 8
US-09-489-039A-2620/c
; Sequence 2620, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2620
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2620

Query Match          75.0%; Score 15; DB 4; Length 1176;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGATGCGCGCGAG 15
        |||||||
        95 ATGATGCGCGCGAG 81

RESULT 9
US-09-270-767-31566/c
; Sequence 31566, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31566
; LENGTH: 1211
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-31566

Query Match          75.0%; Score 15; DB 4; Length 1211;
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GATGCGCGCGAGTG 17
        |||||||
        72 GATGCGCGCGAGTG 58

RESULT 10
US-09-489-039A-2450/c
; Sequence 2450, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2450
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2450

Query Match          75.0%; Score 15; DB 4; Length 1395;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGATGCGCGCGAG 15
        |||||||
        1325 ATGATGCGCGCGAG 1311

RESULT 11
US-09-270-767-15231/c
; Sequence 15231, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15231
; LENGTH: 1498
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-15231

Query Match          75.0%; Score 15; DB 4; Length 1498;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GATGCGCGCGAGTG 17
        |||||||
        72 GATGCGCGCGAGTG 58

RESULT 12
US-09-902-540-3960
; Sequence 3960, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
US-09-902-540-3960
```

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; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3960
; LENGTH: 2118
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3960

Query Match
Best Local Similarity 100.0%; Score 15; DB 4; Length 2118;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GATGGCGCGGAGTG 17
DB 516 GATGGCGCGGAGTG 530

RESULT 13
US-09-902-540-1196
; Sequence 1196, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1196
; LENGTH: 18324
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1196

Query Match
Best Local Similarity 100.0%; Score 15; DB 4; Length 18324;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GATGGCGCGGAGTG 17
DB 3168 GATGGCGCGGAGTG 3182

RESULT 14
US-09-949-016-12617/c
; Sequence 12617, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12617
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; LENGTH: 160018
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(160018)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12617

Query Match
Best Local Similarity 100.0%; Score 15; DB 4; Length 160018;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCGGAGTGTA 20
DB 1171 GGCGGCGGAGTGTA 1157

RESULT 15
US-09-949-016-15994/c
; Sequence 15994, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15994
; LENGTH: 160018
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(160018)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15994

Query Match
Best Local Similarity 100.0%; Score 15; DB 4; Length 160018;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCGGAGTGTA 20
DB 1171 GGCGGCGGAGTGTA 1157
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Search completed: April 12, 2005, 01:20:40
Job time: 128 secs

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Query      1 ATGATGGCGGCAGGTCTGA 20
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Db          1 ATGATGGCGGCAGGTCTGA 20

Matches    20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Query Match      100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.12;
Publication No. US20050026860A1
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; GENERAL INFORMATION:
; APPLICANT: Chin-Tang Lin
; TITLE OF INVENTION: Nucleolin Antisense Sequence FOR Inhibition of CANCER Cell Prolif
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/797,822
; CURRENT FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sense fragment which sequence is similar to the nucleolin mRNA
US-10-797-822-2

Query Match          100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGGAGTGTGA 20
    |||||
Db 20 ATGATGGCGGCGGAGTGTGA 1

RESULT 3
US-10-357-930-35092/C
; Sequence 35092, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endegge, Wilson
; APPLICANT: Morahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35092
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-35092

Query Match          100.0%; Score 20; DB 18; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGGAGTGTGA 20
    |||||
Db 116 ATGATGGCGGCGGAGTGTGA 97

RESULT 4
US-09-918-995-37497/C
; Sequence 37497, Application US/09918995
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37497
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-37497

Query Match          100.0%; Score 20; DB 10; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGGAGTGTGA 20
    |||||
Db 98 ATGATGGCGGCGGAGTGTGA 79

RESULT 5
US-10-357-930-4788/C
; Sequence 4788, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endegge, Wilson
; APPLICANT: Morahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4788
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 224_242, 273, 286, 312, 321
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-4788

Query Match          100.0%; Score 20; DB 18; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGGAGTGTGA 20
    |||||
```

Db 86 ATGATGCGCGGAGTGTA 67

RESULT 6

US-10-357-930-43939/c

Sequence 43939, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-007BCN

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785,276

PRIOR FILING DATE: 2003-02-16

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/189,862

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: 60/255,281

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 62232

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 43939

LENGTH: 438

TYPE: DNA

ORGANISM: Homo sapiens

US-10-357-930-43939

Query Match

Best Local Similarity 100.0%; Score 20; DB 18; Length 438;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGGAGTGTA 20

|||||

Db 80 ATGATGCGCGGAGTGTA 61

|||||

RESULT 7

US-10-357-930-13957/c

Sequence 13957, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-007BCN

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785,276

PRIOR FILING DATE: 2003-02-16

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/189,862

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: 60/255,281

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 62232

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13957

LENGTH: 444

TYPE: DNA

ORGANISM: Homo sapiens

US-10-357-930-13957

Query Match

Best Local Similarity 100.0%; Score 20; DB 18; Length 444;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGGAGTGTA 20

|||||

Db 70 ATGATGCGCGGAGTGTA 51

|||||

RESULT 8

US-10-198-846-9321/c

Sequence 9321, Application US/10198846

Publication No. US20030099974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9321

LENGTH: 636

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: misc_feature

LOCATION: 3, 9, 56, 59

OTHER INFORMATION: n = A,T,C or G

US-10-198-846-9321

Query Match

Best Local Similarity 100.0%; Score 20; DB 14; Length 636;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGGAGTGTA 20

|||||

Db 133 ATGATGCGCGGAGTGTA 114

|||||

RESULT 9

US-10-363-345A-27853

Sequence 27853, Application US/10363345A

Publication No. US20040234960A1

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Method for determining the degree of methylation of defined

TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3

FILE REFERENCE: E01/1227

CURRENT APPLICATION NUMBER: US/10/363,345A

CURRENT FILING DATE: 2003-03-03

NUMBER OF SEQ ID NOS: 40712

SEQ ID NO 27853

LENGTH: 1276
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-27853

Query Match
Best Local Similarity 100.0%; Score 20; DB 18; Length 1276;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGGCGCGGAGTGTGA 20
Db 582 ATGATGGCGCGGAGTGTGA 601

RESULT 10
US-10-363-345A-27854/c
Sequence 27854, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 27854
LENGTH: 1276
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-27854

Query Match
Best Local Similarity 100.0%; Score 20; DB 18; Length 1276;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGGCGCGGAGTGTGA 20
Db 695 ATGATGGCGCGGAGTGTGA 676

RESULT 11
US-10-363-483A-27853
Sequence 27853, Application US/10363483A
Publication No. US20050064401A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 27853
LENGTH: 1276
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-27853

Query Match 100.0%; Score 20; DB 19; Length 1276;

Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGGCGCGGAGTGTGA 20
Db 582 ATGATGGCGCGGAGTGTGA 601

RESULT 12
US-10-363-483A-27854/c
Sequence 27854, Application US/10363483A
Publication No. US20050064401A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 27854
LENGTH: 1276
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-27854

Query Match
Best Local Similarity 100.0%; Score 20; DB 19; Length 1276;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGGCGCGGAGTGTGA 20
Db 695 ATGATGGCGCGGAGTGTGA 676

RESULT 13
US-10-357-930-28900/c
Sequence 28900, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: NRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28900
LENGTH: 1860
TYPE: DNA


```
; ORGANISM: Homo sapiens
US-10-357-930-28900

Query Match          100.0%; Score 20; DB 18; Length 1860;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGATGCGCGCGAGTGTGA 20
        |||||
DB      113 ATGATGCGCGCGAGTGTGA 114

RESULT 14
US-09-825-886-28/C
; Sequence 28, Application US/09825886
; Publication No. US20020076693A1
; GENERAL INFORMATION:
; APPLICANT: Hovanesian, Ara
; APPLICANT: Callebaut, Christian
; APPLICANT: Krust, Bernard
; APPLICANT: Jacotot, Etienne
; APPLICANT: Muller, Sylviane
; APPLICANT: Briand, Jean-Paul
; APPLICANT: Guichard, Gilles
; TITLE OF INVENTION: A NOVEL CELL SURFACE RECEPTOR FOR HIV RETROVIRUSES.
; FILE REFERENCE: 03495.0166-01000
; CURRENT APPLICATION NUMBER: US/09/825,886
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 09/393,302
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/EP98/01409
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,969
; PRIOR FILING DATE: 1997-03-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 2518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-886-28

Query Match          100.0%; Score 20; DB 9; Length 2518;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGATGCGCGCGAGTGTGA 20
        |||||
DB      113 ATGATGCGCGCGAGTGTGA 94

RESULT 15
US-10-400-083-18/C
; Sequence 18, Application US/10400083
; Publication No. US20040186056A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Porkka, Kimmo
; APPLICANT: Christian, Sven
; TITLE OF INVENTION: HMGN2 Peptides and Related Molecules
; TITLE OF INVENTION: that Selectively Home to Tumor Blood Vessels and Tumor Cells
; FILE REFERENCE: P-LJ 5662
; CURRENT APPLICATION NUMBER: US/10/400,083
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 10/116,866
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 2518
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112)...(2235)
US-10-400-083-18

Query Match          100.0%; Score 20; DB 18; Length 2518;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGATGCGCGCGAGTGTGA 20
        |||||
DB      113 ATGATGCGCGCGAGTGTGA 94

Search completed: April 12, 2005, 01:29:20
Job time : 510 secs
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Query Match      100.0%; Score 20; DB 4; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGATGCGCGCGGAGTGTCA 20
        |||||
DB       70 ATGATGCGCGCGGAGTGTCA 89

```

RESULT 2	
CBI27338/c	
LOCUS	142 bp mRNA linear EST 29-JAN-2003
DEFINITION	CB127338 Ct-ESTD176605 C1SNU17 Homo sapiens cDNA clone C1SNU17-9-G05 5', mRNA sequence.
ACCESSION	CB127338
VERSION	CB127338.1 GI:28089748
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 142) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Kim,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
AUTHORS	
TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS

TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 9 row: G column: 05 High quality sequence stop: 142.
FEATURES	Location/Qualifiers
SOURCE	1. 142

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Source
1. 142
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="C15NU17-9-G05"
/sex="F"
/tissue_type="uterine"
/cell_type="Epithelial"
/cell_line="SNV-17"
/lab_host="Top10F"
/clone_id="C15NU17"
/note="Organ: Cervix; Vector: PCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tobacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

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ORIGIN		Query Match	100.0%	Score 20;	DB 6;	Length 142;
		Best Local Similarity	100.0%	Pred. No. 0.34		
	Matches	20; Conservative	0;	Mismatches	0;	Indels
					Gaps	0;
Oy	1	ATGATGGCGCGGAGTGTGA	20			
Db	130	ATGATGGCGCGGAGTGTGA	111			

RESULT 3
AL121075/c
LOCUS
DEFINITION
AL121075 155 bp mRNA linear EST 04-SEP-2003
DKEZP628035.r1.762 (synonym: hmcl2) Homo sapiens cDNA clone
DKEZP628035.5, mRNA sequence.
AL121075
ACCESSION
VERSION
KEYWORDS
EST. AL121075.1 GI:5927076
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 155)
REFERENCE
AUTHORS
Bloecher,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Bloecher, et al.)
TITLE
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS

FEATURES
Ingolstaedter landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;,
sequenced by GSF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp2B035) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Neuherberg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

```

source
1. .155
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp762B035"
/issue_type="melanoma (Melo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/clone_idb="762 (synonym: hmel2)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match      100.0%;   Score 20;   DB 1;   Length 155;
Best Local Similarity 100.0%;   Pred. No. 0.34;
Matches 20;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Cy      1  ATGATGGCGGCGGAGTGTGA 20
|||||
Db      59  ATGATGGCGGCGGAGTGTGA 40

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RESULT	4
LOCUS	BQ319320
DEFINITION	BQ319320 OVO-CIT0583-101100-491-a04 CIT0583 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BQ319320
VERSION	BQ319320.1 GI:20925236
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryotic; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 160) Nagai Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Dias M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsushima,A., Bala,G.S., Simpson,D.H., Bruneisel,A., deOliveira,P.S., Bucher P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.U. and Simpson,A.U.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=QV0&l2=QV0-CT0583-101100-491-a04&l3=2000-11-10&l4=1)
Seq primer: puc 18 forward
High quality sequence start: 55
High quality sequence stop: 95.
Location/Qualifiers

FEATURES

source

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1..160
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0583"
/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 160;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 ATGATGCGCGCGAGTGTA 20
|||||
129 ATGATGCGCGCGAGTGTA 148

Db

RESULT 5 BE719607 163 bp mRNA linear EST 12-SEP-2000
LOCUS BE719607
DEFINITION RC2-HT0861-310700-011-f06 HT0861 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE719607
VERSION BE719607.1 GI:10107872
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 163)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.G.

AUTHORS

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

TITLE

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente, 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC2-HT0861-310700-011-f06&l3=2000-07-31&l4=1)
Seq primer: puc 18 forward
High quality sequence stop: 163.
Location/Qualifiers

FEATURES

source

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1..163
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0861"
/note="Organ: head_neck; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
```

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 ATGATGCGCGCGAGTGTA 20
|||||
114 ATGATGCGCGCGAGTGTA 95

Db

RESULT 6 CN335092 164 bp mRNA linear EST 16-MAY-2004
LOCUS CN335092
DEFINITION 17000532664809 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN335092
VERSION CN335092.1 GI:47335026
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 164)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guejler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.

Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@regeron.com

Insert Length: 164 Std Error: 0.00.

FEATURES

source

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1..164
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="embryonic stem cells, cell lines H1, H7, and H9"
/clone_lib="GRN ES"
/note="Toigo dr-primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"
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ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 164;

Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGCGCGCGAGTGTGA 20
|||||
100 ATGATGCGCGCGAGTGTGA 81

RESULT 7
BE699907/c 178 bp mRNA linear EST 12-SEP-2000

LOCUS MR0-NN0087-230500-009-d06 NN0087 Homo sapiens cDNA, mRNA sequence.

DEFINITION BE699907
VERSION BE699907.1 GI:10087649
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 178)
Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Birones M.R.,
Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,
Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H.,
Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V.,
O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and
Simpson A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

TITLE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE 20202663
PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=et2=MR0-NN0087-230
500-009-d06&t3=2000-05-23&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 178.

FEATURES
source Location/Qualifiers
1..178

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_1b="NN0087"

/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGCGCGCGAGTGTGA 20
|||||
111 ATGATGCGCGCGAGTGTGA 92

RESULT 8
AM575670/c 184 bp mRNA linear EST 15-MAR-2000
LOCUS AM575670

DEFINITION UI-HF-BM0-ack-h-02-0-UI.s1 NIH_MGC_38 Homo sapiens cDNA clone
IMAGE:3062234 3', mRNA sequence.

Qy 1 ATGATGCGCGCGAGTGTGA 20
|||||
77 ATGATGCGCGCGAGTGTGA 58

RESULT 9
AU077224/c 185 bp mRNA linear EST 04-MAY-2000

LOCUS AU077224 Sugano cDNA library Homo sapiens cDNA clone Zrv61966

DEFINITION AU077224 Sugano cDNA library Homo sapiens cDNA clone Zrv61966
similar to 5'-end region of Chinese hamster nucleolin (C23) mRNA,
mRNA sequence.

ACCESSION AU077224
VERSION AU077224.1 GI:7439847
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 184)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Oligo-dt track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. Tissue Procurement: Louis M.
Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bdrrp/image/image.html
Seq primer: M13 Forward
POLYA=No.

FEATURES
source Location/Qualifiers
1..184

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3062234"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTI)"

/clone_1b="NIH MGC 38"

/note="Vector: p773-Pac; Site 1: NcoI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(2.5-3.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 100.0%; Score 20; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGCGCGCGAGTGTGA 20
|||||
77 ATGATGCGCGCGAGTGTGA 58

RESULT 9
AU077224/c 185 bp mRNA linear EST 04-MAY-2000
LOCUS AU077224 Sugano cDNA library Homo sapiens cDNA clone Zrv61966

DEFINITION AU077224 Sugano cDNA library Homo sapiens cDNA clone Zrv61966
similar to 5'-end region of Chinese hamster nucleolin (C23) mRNA,
mRNA sequence.

ACCESSION AU077224
VERSION AU077224.1 GI:7439847
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 185)
Suzuki Y., Ishihara D., Sasaki M., Nakagawa H., Hata H.,
Tanoda T., Watanabe M., Komatsu T., Ota T., Isogai T., Suyama A.
and Sugano S.

Statistical analysis of the 5' untranslated region of human mRNA
using 'Oligo-capped' cDNA libraries
Genomics 64 (3), 286-297 (2000)

MEDLINE
20221373
PUBMED
10756096
COMMENT
Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki Y., Yoshitomo-Nakagawa K., Maruyama K., Suyama A. and
Sugano S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)

FEATURES
source
1.185
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano cDNA library"
Location/Qualifiers

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGCA 20
|||||
Db 137 ATGATGCGCGCGAGTGCA 118

RESULT 10
AW050536/c 205 bp mRNA linear EST 09-MAR-2000
LOCUS w214a01.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2557992 3'
DEFINITION similar to gb:U60858_rnal NCICLROLIN (HUMAN); mRNA sequence.
ACCESSION AW050536
VERSION AW050536.1 GI:5912806
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 205)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
www.bio.lnlnl.gov/bbrp/image/image.html
Insert length: 2161 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 171.
Location/Qualifiers
1..205

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2557992"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ut4"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGCA 20
|||||
Db 57 ATGATGCGCGCGAGTGCA 38

RESULT 11
W79364 210 bp mRNA linear EST 17-OCT-1996
LOCUS zd72dl1.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone
DEFINITION IMAGE:346197 5' similar to gb:U60858_rnal NCICLROLIN (HUMAN); mRNA
sequence.
ACCESSION W79364
VERSION W79364.1 GI:1390153
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 210)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawking, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (lnlnl.gov) for further information.
Insert length: 272 Std Error: 0.00
Seq primer: mob.REGA-ET
Location/Qualifiers
1..210

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1271572"
/db_xref="taxon:9606"
/clone_lib="IMAGE:346197"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBH19W"
/note="Organ: heart; Vector: pRTD3 (pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTCACATCGAAGTGGAGCGCGCCATCTTTTCTTTTCTTTT 3').
double-stranded cDNA was size selected, ligated to Eco RI
adapters (pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRTD3 vector
(pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same focus as the fetal lung library, Soares fetal lung
NBH19W."

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGATGGCGCGGAGTGTGA 20
 |||||
 Db 180 ATGATGGCGCGGAGTGTGA 199

RESULT 12
 LOCUS AA263089/c
 DEFINITION PM26457 KGI-a Lambda Zap Express cDNA library Homo sapiens CDNA 5', mRNA sequence.
 AA263089
 VERSION AA263089.1 GI:1898887
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE Claudio,J.O., Liew,C.C., Dempsey,A.A., Cukerman,E., Stewart,A.K., Na.E., Atkins,H.I., Iscove,N.N. and Hawley,R.G.
 IDENTIFICATION OF SEQUENCE-TAGGED TRANSCRIPTS DIFFERENTIALLY EXPRESSED WITHIN THE HUMAN HEMATOPOIETIC HIERARCHY
 Genomics 50 (1), 44-52 (1998)
 98292493
 MEDLINE
 PUBMED 9628821

COMMENT
 Contact: Hawley RG
 Oncology Research Laboratories
 The Toronto Hospital
 CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
 Tel: 416 3403834
 Fax: 416 3403453
 Email: r.hawley@utoronto.ca
 Similar to M60858 nucleolin gene. Clone was randomly picked from Kgi primary library.
 Seq primer: 5' GAATTTACCTTCCTACTAAAGG 3'
 High quality sequence stop: 215.
 Location/Qualifiers
 1..215
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_type="promyeloblast"
 /clone_lib="KGI-a"
 /note="Vector: Lambda Zap Express (Stratagene); Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning sites: EcoRI-XhoI. mRNA was purified from KGI-a cell line. cDNA was synthesized using an XhoI-0150cdT linker primer. EcoRI adaptors were ligated, followed by digestion with XhoI for directional cloning into predigested Lambda Zap Express"

ORIGIN
 Query Match 100.0%; Score 20; DB 1; Length 215;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGATGGCGCGGAGTGTGA 20
 |||||
 Db 85 ATGATGGCGCGGAGTGTGA 66

RESULT 13
 LOCUS BX644913/c
 DEFINITION DKZP78111236_r1 781 (synonym: hlc4) Homo sapiens cDNA clone
 DKZP78111236 5', mRNA sequence.
 BX644913
 VERSION BX644913.1 GI:34479246
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE Wambutt,R., Heubner,D., Mewes,H.W., Well,B., Amid,C., Osanger,A., Fodor,G., Han,W. and Wiemann,S.
 EST (Wambutt,R., Heubner,D., Mewes,H.W., Well,B., Amid,C., et al.)
 Unpublished (2003)
 COMMENT
 Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No sl sequence available.
 This clone (DKZP78111236) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcententrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
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 1..219
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
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 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="781 (synonym: hlc4)"
 /note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

ORIGIN
 Query Match 100.0%; Score 20; DB 5; Length 219;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGATGGCGCGGAGTGTGA 20
 |||||
 Db 119 ATGATGGCGCGGAGTGTGA 100

RESULT 14
 LOCUS BF757253
 DEFINITION OV0-CT0583-031100-476-e03 CT0583 Homo sapiens cDNA, mRNA sequence.
 BF757253
 VERSION BF757253.1 GI:12105153
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 220)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsubara,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.V. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 JOURNAL
 MEDLINE
 PUBMED 10737800

COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LIRC Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV0&c2=QV0-CT0583-03100-476-e03&c3=2000-11-03&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 220.
Location/Qualifiers

FEATURES

source

1..220
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1ib="CT0583"
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20
|||||
Db 189 ATGATGCGCGCGAGTGTGA 208

RESULT 15
A1185752/c 221 bp mRNA linear EST 29-OCT-1998
LOCUS qe44e01.x1 Soares fetal_lung_NbHL19w Homo sapiens cDNA clone
DEFINITION IMAGE:1741848 3' similar to gb:M60858_rna1 NUCLEOLIN (HUMAN); mRNA
sequence.

ACCESSION A1185752

VERSION A1185752

KEYWORDS A1185752.1 GI:3736390

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

TITLE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL NCI-CCAP National Cancer Institute, Cancer Genome/Anatomy Project (CGAP),
Tumor Gene Index

COMMENT Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-r@mail.nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 954 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 182.

Location/Qualifiers

1..221

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1741848"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/clone_1ib="Soares_fetal_lung_NbHL19w"

/note="Organ: lung; Vector: pT773D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT773 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 221;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20
|||||
Db 37 ATGATGCGCGCGAGTGTGA 18

Search completed: April 12, 2005, 01:18:23
Job time : 3107 secs

Soares and M. Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19w."

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 11, 2005, 21:24:33 ; Search time 1674 Seconds
(without alignments)
578.915 Million cell updates/sec

Title: US-10-797-822-1

Perfect score: 20

Sequence: 1 atgatgcgcgcgcgagtgctga 20

Scoring table: **OMEGA NUC**
Gapop 60.0 , Gapect 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmb1:*

1: gb_ba:.*
2: gb_htg:.*
3: gb_in:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pac:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_ey:.*
13: gb_un:.*
14: gb_vl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	240	6	CQ503225 Sequence
2	20	100.0	396	6	CQ472921 Sequence
3	20	100.0	438	6	CQ512072 Sequence
4	20	100.0	442	6	AR421707 Sequence
5	20	100.0	442	6	AX982401 Sequence
6	20	100.0	442	6	BD117260 Sequence
7	20	100.0	444	6	CQ482090 Sequence
8	20	100.0	467	6	AX885265 Sequence
9	20	100.0	467	6	BD024875 Sequence
10	20	100.0	620	9	HS338862 Homo sapi
11	20	100.0	643	9	HS339439 Homo sapi
12	20	100.0	716	9	HS339590 Homo sapi
13	20	100.0	788	9	HS342352 Homo sapi
14	20	100.0	863	9	HS342353 Homo sapi
15	20	100.0	1860	6	CQ497033 Sequence
16	20	100.0	1952	9	BC002343 Homo sapi
17	20	100.0	1957	9	BC006494 Homo sapi
18	20	100.0	1957	9	BC006516 Homo sapi
19	20	100.0	2084	6	CQ725884 Sequence

C 20	20	100.0	2400	6	CQ850470 Sequence
C 21	20	100.0	2400	9	AK127608 Homo sapi
C 22	20	100.0	2542	9	AK000221 Homo sapi
C 23	20	100.0	2560	9	AK095897 Homo sapi
C 24	20	100.0	2637	6	AX747156 Sequence
C 25	20	100.0	2637	9	AK091742 Homo sapi
C 26	20	100.0	2655	9	AK122805 Homo sapi
C 27	20	100.0	3201	6	CQ490280 Sequence
C 28	20	100.0	3201	6	CQ491168 Sequence
C 29	20	100.0	6112	6	AX347419 Sequence
C 30	20	100.0	6112	6	AX349140 Sequence
C 31	20	100.0	6112	6	AX657789 Sequence
C 32	20	100.0	6112	6	AX659063 Sequence
C 33	20	100.0	10942	9	HUMANUCLEO
C 34	20	100.0	16880	9	AC017104 Homo sapi
C 35	20	100.0	134014	8	AC137698 Genomic s
C 36	18	90.0	187589	8	AC083942 Genomic s
C 37	17	85.0	109148	2	AC138439 Takifugu
C 38	17	85.0	110000	2	AC021644_0 Homo sapi
C 39	17	85.0	129040	8	AP005466 Oryza sat
C 40	17	85.0	157822	8	AP004731 Oryza sat
C 41	16	80.0	11349	2	AC012868 Drosophila
C 42	16	80.0	11629	1	AE010310 Methanopy
C 43	16	80.0	19653	1	AF299336 Stigmatal
C 44	16	80.0	84055	3	AC004439 Drosophila
C 45	16	80.0	138715	8	OSJN00190 Oryza sat

ALIGNMENTS

RESULT 1	CQ503225/c	Sequence 35092 from Patent WO0160860.	240 bp	DNA	linear	PAT 30-JAN-2004
LOCUS	CQ503225					
DEFINITION	CQ503225					
ACCESSION	CQ503225					
VERSION	CQ503225.1	GI:41468861				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens	(human)				
REFERENCE						
AUTHORS	Schlegel, R., Endege, W.O. and Monahan, J.E.					
TITLE	Genes differentially expressed in human prostate cancer and their use					
JOURNAL	Patent: WO 0160860-A 35092 23-AUG-2001;					
FEATURES	Millennium Predictive Medicine, Inc. (US)					
source	1..240	Location/Qualifiers				
	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
ORIGIN						
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Best Local Similarity	100.0%;	Pred. No. 3.9;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ATGATGCGCGCGAGTGTA	20			
Db	116	ATGATGCGCGCGAGTGTA	97			
RESULT 2	CQ472921/c	Sequence 4788 from Patent WO0160860.	396 bp	DNA	linear	PAT 30-JAN-2004
LOCUS	CQ472921					
DEFINITION	CQ472921					
ACCESSION	CQ472921					
VERSION	CQ472921.1	GI:41438540				
KEYWORDS						
SOURCE	Homo sapiens	(human)				
ORGANISM	Homo sapiens					

REFERENCE 1
AUTHORS Schlegel R., Endege, W.O. and Monahan, J.B.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 4788 23-AUG-2001;
FEATURES Millennium Predictive Medicine, Inc. (US)
source Location/Qualifiers
1.396
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 100.0%; Pred. No. 3.7; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 ATGATGCGCGCGAGTGTGA 20
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86 ATGATGCGCGCGAGTGTGA 67

RESULT 3
COSI1072/c 438 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 43939 from Patent WO0160860.
DEFINITION COSI2072
ACCESSION COSI2072.1 GI:41478336
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.B.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 43939 23-AUG-2001;
FEATURES Millennium Predictive Medicine, Inc. (US)
source Location/Qualifiers
1.438
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.7; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 ATGATGCGCGCGAGTGTGA 20
|||
80 ATGATGCGCGCGAGTGTGA 61

RESULT 4
AR421707 442 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 13204 from patent US 6639063.
DEFINITION AR421707
ACCESSION AR421707.1 GI:40176817
VERSION
KEYWORDS
SOURCE
ORGANISM Unknown.
Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 442)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.-Y.
TITLE EST's and encoded human protein
JOURNAL Patent: US 6639063-A 13204 28-OCT-2003;
FEATURES Location/Qualifiers
1.442
source

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.7; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 ATGATGCGCGCGAGTGTGA 20
|||
166 ATGATGCGCGCGAGTGTGA 147

RESULT 5
AX982401/c 442 bp DNA linear PAT 15-JAN-2004
LOCUS Sequence 13204 from Patent EP1104808.
DEFINITION AX982401
ACCESSION AX982401.1 GI:40988541
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.-Y.
TITLE ESTs and encoded human proteins
JOURNAL Patent: EP 1104808-A 13204 06-JUN-2001;
FEATURES Genset (FR)
source Location/Qualifiers
1.442
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.7; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 ATGATGCGCGCGAGTGTGA 20
|||
166 ATGATGCGCGCGAGTGTGA 147

RESULT 6
BD117260/c 442 bp DNA linear PAT 18-SEP-2002
LOCUS EST and encoded human protein.
DEFINITION BD117260
ACCESSION BD117260.1 GI:23212164
VERSION JP 2002010789-A/9337.
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 442)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.-Y.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 9337 15-JAN-2002;
FEATURES GENSET CORP
source OS Homo sapiens (human)
PN JP 2002010789-A/9337
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein

FEATURES
source
1.442
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Query Match 100.0%; Score 20; DB 6; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20
|||||
166 ATGATGGCGCGGAGTGTGA 147

RESULT 7
LOCUS CQ482090 444 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 13957 from Patent WO0160860.
ACCESSION CQ482090
VERSION CQ482090.1 GI:41447709
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
JOURNAL use
Patent: WO 0160860-A 13957 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
LOCATION/Qualifiers
1.444
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 444;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20
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70 ATGATGGCGCGGAGTGTGA 51

RESULT 8
LOCUS AX885265/c 467 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1128 from Patent EP1033401.
ACCESSION AX885265
VERSION AX885265.1 GI:40041253
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Dumas Milne Edwards, J.B., Duclet, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 1128 06-SEP-2000;
Genet (FR)
LOCATION/Qualifiers
1.467
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source

CDS 162..>467
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/codon_start=1
/protein_id="CAE99379.1"
/db_xref="GI:40041254"
/translation="MVKLAKAGKNGDPPKRAAPPKEVEEDSEDEMSDEDDSSGE
EVVLPQKGGKKAATSAKKVVSPTKVAVAATPAKAAVTPGKAAATPAKKTVPKAK
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20
|||||
163 ATGATGGCGCGGAGTGTGA 144

RESULT 9
LOCUS BD024875/c 467 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD024875
VERSION BD024875.1 GI:22566098
KEYWORDS JP 2001269182-A/1121.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE 1 (bases 1 to 467)
JOURNAL Sequence tag and encoded human protein
Patent: JP 2001269182-A 1121 02-OCT-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/1121
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JUAN BAPOTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40

CC
FH Key Location/Qualifiers
FT CDS 162..467.
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1.467
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Query Match 100.0%; Score 20; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20
|||||
163 ATGATGGCGCGGAGTGTGA 144

RESULT 10
LOCUS HSA338862/c 620 bp DNA linear PRI 18-JUL-2002
DEFINITION Homo sapiens genomic sequence surrounding Nct1 site, clone
ACCESSION HSA338862
VERSION AJ338862
KEYWORDS AJ338862.1 GI:15883280

FEATURES
source

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SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 620)
AUTHORS     Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvaasha,S.M.,
            Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
            Levitsky,V.G., Kolchanov,N.A., Protodopov,A.I., Kashuba,V.I.,
            Kiselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
            NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
TITLE       Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL     Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE     22131767
PUBMED      12136098
REFERENCE   2 (bases 1 to 620)
AUTHORS     Zabarovsky,E.R.
            Direct Submission
TITLE       Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES    source
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            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="NLI-UP5C"
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Best Local Similarity 100.0%; Pred. No. 3.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Cy 1 ATGATGGCGCGGAGTGTGA 20
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78 ATGATGGCGCGGAGTGTGA 59

RESULT 11
HSA339439      643 bp      DNA      linear      PRI 18-JUL-2002
LOCUS          HSA339439
DEFINITION     Homo sapiens genomic sequence surrounding NotI site, clone
NRI-MASC.
ACCESSION     AJ339439
VERSION       AJ339439.1 GI:15883857
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 643)
AUTHORS     Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvaasha,S.M.,
            Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
            Levitsky,V.G., Kolchanov,N.A., Protodopov,A.I., Kashuba,V.I.,
            Kiselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
            NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
TITLE       Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL     Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE     22131767
PUBMED      12136098
REFERENCE   2 (bases 1 to 643)
AUTHORS     Zabarovsky,E.R.
            Direct Submission
TITLE       Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES    source
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            /clone="NRI-MASC"
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Cy 1 ATGATGGCGCGGAGTGTGA 20
    ||||||||||||||||
78 ATGATGGCGCGGAGTGTGA 59

RESULT 12
HSA339590      716 bp      DNA      linear      PRI 18-JUL-2002
LOCUS          HSA339590
DEFINITION     Homo sapiens genomic sequence surrounding NotI site, clone
NLI-Z021C.
ACCESSION     AJ339590
VERSION       AJ339590.1 GI:15884008
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 716)
AUTHORS     Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvaasha,S.M.,
            Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
            Levitsky,V.G., Kolchanov,N.A., Protodopov,A.I., Kashuba,V.I.,
            Kiselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
            NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
TITLE       Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL     Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE     22131767
PUBMED      12136098
REFERENCE   2 (bases 1 to 716)
AUTHORS     Zabarovsky,E.R.
            Direct Submission
TITLE       Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES    source
            1..716
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="NLI-Z021C"
ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 716;
Best Local Similarity 100.0%; Pred. No. 3.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Cy 1 ATGATGGCGCGGAGTGTGA 20
    ||||||||||||||||
78 ATGATGGCGCGGAGTGTGA 59

RESULT 13
HSA342352      788 bp      DNA      linear      PRI 18-JUL-2002
LOCUS          HSA342352
DEFINITION     Homo sapiens genomic sequence surrounding NotI site, clone
NRI-OE8C.
ACCESSION     AJ342352
VERSION       AJ342352.1 GI:15886769
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 788)
AUTHORS     Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvaasha,S.M.,
            Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
            Levitsky,V.G., Kolchanov,N.A., Protodopov,A.I., Kashuba,V.I.,
            Kiselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
            NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
TITLE

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JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 788)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submision
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbilogy Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/clone="NR1-OE8C"

ORIGIN
Query Match- 100.0%; Score 20; DB 9; Length 788;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20
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78 ATGATGCGCGCGAGTGTGA 59

Db

RESULT 14
HSA342353/c 863 bp DNA linear PRI 18-JUL-2002
LOCUS HSA342353
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
NR1-OI12C.
ACCESSION AJ342353
VERSION AJ342353.1 GI:15886770
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 863)
AUTHORS Kuzenko,A.S., Glazulin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,
Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I.,
Kiselev,L.L., Maersman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 863)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submision
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbilogy Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NR1-OI12C"

ORIGIN
Query Match- 100.0%; Score 20; DB 9; Length 863;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20
|||||
78 ATGATGCGCGCGAGTGTGA 59

Db

RESULT 15
CQ497033/c

LOCUS CQ497033 1860 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 28900 from Patent WO0160860.
ACCESSION CQ497033
VERSION CQ497033.1 GI:41462669
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 28900 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
1..1860
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match- 100.0%; Score 20; DB 6; Length 1860;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20
|||||
133 ATGATGCGCGCGAGTGTGA 114

Db

Search completed: April 12, 2005, 00:24:54
Job time : 1678 secs

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Result	Score	Query	Match	Length	DB	ID	Description
C 1	20	100.0	240	5	ABV35074	ABV35074 Human pro	
C 2	20	100.0	377	9	ACH50285	ACH50285 Human lru	
C 3	20	100.0	396	5	ABV04797	ABV04797 Human pro	
C 4	20	100.0	438	5	ABV43920	ABV43920 Human pro	
C 5	20	100.0	444	5	ABV13966	ABV13966 Human pro	
C 6	20	100.0	467	3	AC01130	AC01130 Human sec	
C 7	20	100.0	636	1	ACN88171	ACN88171 Breast can	
C 8	20	100.0	1276	6	ABO41262	ABO41262 Oligonuc1	
C 9	20	100.0	1276	6	ABO41263	ABO41263 Oligonuc1	
C 10	20	100.0	1716	12	ADP46512	ADP46512 Human pro	
C 11	20	100.0	1860	5	ABV28882	ABV28882 Human pro	
C 12	20	100.0	2345	12	ADP46511	ADP46511 Human col	
C 13	20	100.0	2400	13	ADR07433	ADR07433 Full leng	
C 14	20	100.0	2518	2	AAV71745	AAV71745 Human V3	
C 15	20	100.0	2518	4	AAC92553	AAC92553 Human nuc	
C 16	20	100.0	2518	8	ACC61089	ACC61089 Human nuc	
C 17	20	100.0	2518	10	ADD49219	ADD49219 Human nuc	
C 18	20	100.0	2518	13	ADP54085	ADP54085 Human pro	
C 19	20	100.0	2527	13	ACN37850	ACN37850 Tumour-as	
C 20	20	100.0	2637	10	ADB62527	ADB62527 Human CDN	

C	21	20	100.0	2723	12	ADJ58976	AdJ58976 Human nuc
C	22	20	100.0	3201	5	ABV22156	ABV22156 Human pro
C	23	20	100.0	3201	5	ABV23046	ABV23046 Human pro
C	24	20	100.0	3497	11	ACN91991	ACN91991 Breat cd
C	25	20	100.0	6112	6	ABK31981	ABK31981 Human DNA
C	26	20	100.0	6112	8	ADA20369	ADA20369 Prostate
C	27	20	100.0	6112	8	ADA84176	ADA84176 Human ren
C	28	20	100.0	10942	2	AAV71742	AAV71742 Human V3
C	29	20	100.0	10942	12	ADJ58975	AdJ58975 Human nuc
C	30	18	90.0	20	4	AAC92564	AAC92564 Human nuc
C	31	16	80.0	110000	11	ADM27081_00	ADM27081 Hyetherthe
C	32	16	80.0	110000	11	ADM27081_01	Continuation (2 of
C	33	15	75.0	33	11	ADM68394	ADM68394 PER prime
C	34	15	75.0	396	2	AAx21244	Aax21244 C.dactylo
C	35	15	75.0	597	10	ADH84236	Adh84236 Enterococo
C	36	15	75.0	679	3	AAC44545	AAC44545 Zee may
C	37	15	75.0	725	6	ABQ27500	ABQ27500 Oligonuc1
C	38	15	75.0	725	6	ABQ27501	ABQ27501 Oligonuc1
C	39	15	75.0	725	6	ABQ33570	ABQ33570 Oligonuc1
C	40	15	75.0	726	6	ABQ33571	ABQ33571 Oligonuc1
C	41	15	75.0	823	10	ABX74204	ABx74204 Corn part
C	42	15	75.0	1107	8	ACC00659	ACC00659 Oryza sat
C	43	15	75.0	1107	10	ADC33546	Adc33546 cDNA encod
C	44	15	75.0	1173	6	ABQ53192	ABq53192 Oligonuc1
C	45	15	75.0	1173	6	ABQ53193	ABq53193 Oligonuc1

ALIGNMENTS

RESULT 1	
ABV35074/c	
ID	ABV35074 standard; cDNA; 240 BP.
XX	
AC	ABV35074;
XX	
XX	16-SEP-2002 (first entry)
D7	
XX	
DE	Human prostate expression marker cDNA 35065.
XX	
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW	pharmacogenomic marker; gene; ss.
XX	
OS	Homo sapiens.
XX	
XX	WO200160860-A2.
PN	
XX	
PD	23-AUG-2001.
XX	
XX	
PF	20-FEB-2001, 2001WO-US005171.
XX	
PR	17-FEB-2000, 2000US-0183319P.
PR	16-MAR-2000, 2000US-0189862P.
PR	25-MAY-2000, 2000US-0207454P.
PR	09-JUN-2000, 2000US-0211314P.
PR	18-JUL-2000, 2000US-0219007P.
PR	13-DEC-2000, 2000US-0255281P.
XX	
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX	
PI	Schlegel R, Endege WO, Monahan JE;
XX	
DR	WPI, 2001-662795/76.
XX	
PT	Novel isolated nucleic acid molecule associated with cancerous state of
PT	prostate cells and correlating with presence of prostate cancer, useful
PT	for detecting presence of prostate cancer, stage of prostate cancer.
XX	
PS	Claim 1; Page 7324; 11750pp; English.
XX	

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether

CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 CC
 XX Sequence 240 BP; 65 A; 61 C; 66 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 240;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGGCGCGGAGTGTGA 20
 |||||
 Db 116 ATGATGGCGCGGAGTGTGA 97

RESULT 2
 ACH50285/C
 ID ACH50285 standard; cDNA, 377 BP.

ACH50285;

13-OCT-2003 (first entry)

Human leukocyte cDNA #1879.

Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 genome mapping; biodiversity; genetic disorder.

Homo sapiens.

US2003073623-A1.

17-APR-2003.

30-JUL-2001; 2001US-00918995.

30-JUL-2001; 2001US-00918995.

(DRMA/) DRMANAC R T.

(STAC/) STACHE-CRAIN B.

(DICK/) DICKSON M C.

(JONE/) JONES L W.

Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

WPI; 2003-615964/58.

New polynucleotide sequences obtained from various cDNA libraries, useful
 as hybridization probes, as oligomers for PCR, for chromosome and gene
 mapping, in the recombinant production of protein, or in generating
 antisense DNA or RNA.

Claim 1; SEQ ID NO 37497; 44bp; English.

The invention relates to an isolated polynucleotide comprising any one of
 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 determined by the technique of SBH (sequencing by hybridisation). Also
 included is a purified polypeptide comprising a sequence corresponding to
 a reading frame of the novel polynucleotide. The nucleic acid sequences
 are useful in diagnostic as expressed sequence tags (EST) for
 identifying expressed genes or for physical mapping of the human genome,
 in forensics, in assessing biodiversity, or in identifying mutations
 responsible for genetic disorders and other traits. The nucleotide
 sequences are also useful as hybridisation probes, as oligomers for PCR,
 for chromosome and gene mapping, in the recombinant production of
 protein, or in generating antisense DNA or RNA. The purified polypeptide

CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030073623
 CC
 XX Sequence 377 BP; 114 A; 102 C; 98 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGGCGCGGAGTGTGA 20
 |||||
 Db 98 ATGATGGCGCGGAGTGTGA 79

RESULT 3
 ABV04797/C
 ID ABV04797 standard; cDNA, 396 BP.

ABV04797;

13-SEP-2002 (first entry)

Human prostate expression marker cDNA 4788.

Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 pharmacogenomic marker; gene; ss.

Homo sapiens.

WO200160860-A2.

23-AUG-2001.

20-FEB-2001; 2001WO-US005171.

17-FEB-2000; 2000US-0183139P.

16-MAR-2000; 2000US-0189862P.

25-MAY-2000; 2000US-0207454P.

09-JUN-2000; 2000US-0211314P.

18-JUL-2000; 2000US-0219007P.

13-DEC-2000; 2000US-0255281P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of
 prostate cells and correlating with presence of prostate cancer. Useful
 for detecting presence of prostate cancer, stage of prostate cancer.

Claim 1; Page 824-825; 11750bp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising
 a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 specification or its complement. (I) is useful for: (a) assessing whether
 a patient is afflicted with prostate cancer; (b) monitoring the efficacy
 of progression of prostate cancer in a patient; (c) assessing the efficacy
 of a test compound to inhibit prostate cancer in a patient; (d) assessing
 the efficacy of a therapy for inhibiting prostate cancer in a patient;
 (e) selecting a composition for inhibiting prostate cancer in a patient;
 (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 determining whether prostate cancer has metastasized in a patient; (h)
 assessing the aggressiveness or indolence of prostate cancer in a patient
 ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

Sequence 396 BP; 125 A; 94 C; 103 G; 68 T; 0 U; 6 Other;

Query Match 100.0%; Score 20; DB 5; Length 396;

Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGATGCGCGCGAGTGTGA 20
|||||
DB 86 ATGATGCGCGCGAGTGTGA 67

RESULT 4
ABV43920/c
ID ABV43920 standard; cDNA; 438 BP.

XX ABV43920;

XX 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 43911.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

XX 17-FEB-2000; 2000US-0183119P.

XX 16-MAR-2000; 2000US-0189862P.

XX 25-MAY-2000; 2000US-0207454P.

XX 09-JUN-2000; 2000US-0211314P.

XX 18-JUL-2000; 2000US-0219007P.

XX 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of

XX prostate cells and correlating with presence of prostate cancer, useful

XX for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 8734; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising

XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

XX specification or its complement. (I) is useful for: (a) assessing whether

XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy

XX of a test compound to inhibit prostate cancer in a patient; (c) assessing the efficacy

XX of a test compound to inhibit prostate cancer in a patient; (d) assessing

XX the efficacy of a therapy for inhibiting prostate cancer in a patient;

XX (e) selecting a composition for inhibiting prostate cancer in a patient;

XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)

XX determining whether prostate cancer has metastasized in a patient; (h)

XX assessing the aggressiveness or indolence of prostate cancer in a patient

XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 438 BP; 140 A; 113 C; 118 G; 67 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 5; Length 438;

XX Best Local Similarity 100.0%; Pred. No. 0.19;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 ATGATGCGCGCGAGTGTGA 20

XX |||||||

XX DB 80 ATGATGCGCGCGAGTGTGA 61

XX RESULT 5

ABV13966/c
ID ABV13966 standard; cDNA; 444 BP.

XX ABV13966;

XX 13-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 13957.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

XX 17-FEB-2000; 2000US-0183119P.

XX 16-MAR-2000; 2000US-0189862P.

XX 25-MAY-2000; 2000US-0207454P.

XX 09-JUN-2000; 2000US-0211314P.

XX 18-JUL-2000; 2000US-0219007P.

XX 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of

XX prostate cells and correlating with presence of prostate cancer, useful

XX for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 2327; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising

XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

XX specification or its complement. (I) is useful for: (a) assessing whether

XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy

XX of a test compound to inhibit prostate cancer in a patient; (c) assessing the efficacy

XX of a test compound to inhibit prostate cancer in a patient; (d) assessing

XX the efficacy of a therapy for inhibiting prostate cancer in a patient;

XX (e) selecting a composition for inhibiting prostate cancer in a patient;

XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)

XX determining whether prostate cancer has metastasized in a patient; (h)

XX assessing the aggressiveness or indolence of prostate cancer in a patient

XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 444 BP; 151 A; 114 C; 111 G; 68 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 5; Length 444;

XX Best Local Similarity 100.0%; Pred. No. 0.19;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 ATGATGCGCGCGAGTGTGA 20

XX |||||||

XX DB 70 ATGATGCGCGCGAGTGTGA 51

XX RESULT 6

XX AAC01130/c

XX ID AAC01130 standard; cDNA; 467 BP.

XX AAC01130;

XX 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 1128.

XX DE

XX XX

KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping; ss.
 XX Homo sapiens.
 XX EP1033401-A2.
 PN 06-SEP-2000.
 XX 21-FEB-2000; 2000EP-00200610.
 PF 26-FEB-1999; 99US-0122487P.
 XX (GEST) GENSET.
 PA Dumas Milne Edwards J, Duclert A, Giordano J;
 PI WPI; 2000-500381/45.
 XX P-PSDB; AAG01124.
 DR New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX Claim 1; SEQ ID NO 1128; 71bp + Sequence Listing; English.
 PS The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. An ORF has been identified within the
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 CC derived from 30 different tissues. EST sequences usually correspond
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
 CC well suited for isolating cDNA sequences derived from the 5' ends of
 CC mRNAs and even in those cases where longer cDNA sequences have been
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
 CC gene therapy and chromosome mapping procedures. They are used to obtain
 CC upstream regulatory sequences and to design expression and secretion
 CC vectors
 CC
 SQ Sequence 467 BP; 133 A; 127 C; 123 G; 84 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 3; Length 467;
 Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGATGGCGGCGAGTGTGA 20
 Db 163 ATGATGGCGGCGAGTGTGA 144
 RESULT 7
 ID ACN88171/C
 ACN88171 standard; DNA; 636 BP.
 ACN88171;
 DT 02-DEC-2004 (first entry)
 XX Breast cancer related marker, seq id 9321.
 DE Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
 XX Homo sapiens.
 OS US2003099974-A1.
 PN 29-MAY-2003.
 PD 18-JUL-2002; 2002US-00198846.
 PF 18-JUL-2001; 2001US-0306220P.
 PR

XX (MILL-) MILLENNIUM PHARM INC.
 PA Lillie J, Xu Y, Wang Y, Steinmann K;
 XX WPI; 2003-787014/74.
 DR Novel isolated polypeptide associated with breast cancer, useful for
 PT detecting presence of polypeptide in sample, as a marker for breast
 PT cancer.
 XX Disclosure; SEQ ID NO 9321; 36pp; English.
 PS The invention relates to an isolated polypeptide (I) associated with
 CC breast cancer which is encoded by a nucleic acid molecule comprising a
 CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
 CC the polypeptide of the invention. The activity of the polypeptide of the
 CC invention may be described as cytostatic. The antibody is useful for
 CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
 CC invention are useful in the detection of breast tumours. (I) is useful as
 CC a marker for breast cancer and in breast cancer therapy. Sequences given
 CC in records ACN78851-ACN92934 represent nucleic acid markers associated
 CC with breast cancer. Note: The sequence listing does not form part of the
 CC specification but may be obtained in electronic format from the USPTO web
 CC site at seqdata.uspto.gov/sequence.html?docID=20030099974
 CC
 SQ Sequence 636 BP; 205 A; 144 C; 180 G; 103 T; 0 U; 4 Other;
 Query Match 100.0%; Score 20; DB 11; Length 636;
 Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGATGGCGGCGAGTGTGA 20
 Db 133 ATGATGGCGGCGAGTGTGA 114
 RESULT 8
 ID ABQ41262
 ABQ41262 standard; DNA; 1276 BP.
 ACN881262;
 DT 12-JUL-2002 (first entry)
 XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 27853.
 DE Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KM drug; side effect; cancer; central nervous system; cardiovascular;
 KM gastrointestinal; respiratory system; single nucleotide polymorphism;
 KM SNP; cell differentiation; ds.
 XX Homo sapiens.
 OS WO200218632-A2.
 PN 07-MAR-2002.
 PD 01-SEP-2001; 2001WO-EP010074.
 PF 01-SEP-2000; 2000DE-01043826.
 PR 05-SEP-2000; 2000DE-01044543.
 XX (EPIC-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K, Guetig D;
 PI WPI; 2002-371829/40.
 DR Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.
 XX

PS Claim 12; 56bp + Sequence Listing; 56bp; German.
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridized to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridization to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridized to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's) and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
SQ Sequence 1276 BP; 205 A; 151 C; 442 G; 478 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 1276;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGCGCGCGAGTGTGA 20
DB 582 ATGATGCGCGCGAGTGTGA 601
|||||
RESULT 9
ABQ41263/C
ID ABQ41263 standard; DNA; 1276 BP.
XX
AC ABQ41263;
XX
DT 12-JUN-2002 (first entry)
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27854.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
FN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PE 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56bp + Sequence Listing; 56bp; German.
XX This invention describes a novel method for determining the degree of

CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridized to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridization to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridized to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's) and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
SQ Sequence 1276 BP; 478 A; 442 C; 151 G; 205 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 1276;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGCGCGCGAGTGTGA 20
DB 695 ATGATGCGCGCGAGTGTGA 676
|||||
RESULT 10
ADP46512/C
ID ADP46512 standard; DNA; 1716 BP.
XX
AC ADP46512;
XX
DT 09-SEP-2004 (first entry)
DE Human colon specific nucleic acid SEQ ID NO:88.
XX
KW ds; gene; human; colon specific protein; CSP; CSNA; cytostatic; vaccine;
KW gene therapy; colon specific nucleic acid; cancer; colon;
KW chromosome 2q37.1.
XX
OS Homo sapiens.
XX
FN WO2004050860-A2.
XX
PD 17-JUN-2004.
XX
PF 04-DEC-2003; 2003WO-US040063.
XX
PR 04-DEC-2002; 2002US-0431132P.
PR 04-DEC-2002; 2002US-0431144P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Turner LR, Sun Y;
XX
DR WPI; 2004-480623/45.
XX
PT Novel colon specific protein derived from normal and neoplastic colon
PT cell, useful as vaccine in treating colon cancer and in identifying,
PT diagnosing, monitoring, staging, imaging colon cancer and non-cancerous
PT disease state in colon.
XX
PS Claim 1; SEQ ID NO 88; 547bp; English.
XX
XX The invention relates to a novel colon specific protein (CSP) (1) and the
CC nucleic acid (CSNA) encoding it. A CSP of the invention has cytostatic
CC activity. The protein is useful as a vaccine, and the nucleic acid may
CC have a use in gene therapy. A CSP is useful for determining the presence

CC of a colon specific protein in a sample. A CSNA is useful for determining
 CC the presence of a colon specific nucleic acid (CSNA) in a sample. The CSP
 CC and CSNA are useful for diagnosing or monitoring the presence and
 CC metastases of colon cancer in a patient. A method of the invention is
 CC useful for treating a patient with colon cancer. A CSP and CSNA are
 CC useful in identifying, diagnosing, monitoring, staging, imaging colon
 CC cancer and non-cancerous disease state in colon, and as a vaccine for
 CC treating colon cancer and non-cancerous disease states in colon. The
 CC present sequence represents a CSNA of the invention.

XX Sequence 1716 BP; 592 A; 324 C; 486 G; 314 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 1716;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGAGTGTGA 20
 DB 152 ATGATGGCGGCGAGTGTGA 133

RESULT 11

ABV28882/c
 ID ABV28882 standard; cDNA; 1860 BP.

XX ABV28882;

XX 16-SEP-2002 (first entry)

XX Human prostate expression marker CDNA 28873.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

XX 17-FEB-2000; 2000US-0183139P.

XX 16-MAR-2000; 2000US-0189863P.

XX 25-MAY-2000; 2000US-0207454P.

XX 09-JUN-2000; 2000US-0211314P.

XX 18-JUL-2000; 2000US-0215007P.

XX 13-DEC-2000; 2000US-0255281P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 6089; 11750P; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 1860 BP; 572 A; 359 C; 462 G; 467 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 1860;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGAGTGTGA 20
 DB 133 ATGATGGCGGCGAGTGTGA 114

RESULT 12

ADP46511/c
 ID ADP46511 standard; DNA; 2345 BP.

XX ADP46511;

XX 09-SEP-2004 (first entry)

XX Human colon specific nucleic acid SEQ ID NO:87.

XX ds; gene; human; colon specific protein; CSP; CSNA; cytostatic; vaccine;
 KW gene therapy; colon specific nucleic acid; cancer; colon;

XX Chromosome 2q37.1.

XX Homo sapiens.

XX WO2004050860-A2.

XX 17-JUN-2004.

XX 04-DEC-2003; 2003WO-US040063.

XX 04-DEC-2002; 2002US-0431132P.

XX 04-DEC-2002; 2002US-0431144P.

XX (DIAD-) DIADEXUS INC.

XX Macina RA, Turner LR, Sun Y;

XX WPI; 2004-480623/45.

XX Novel colon specific protein derived from normal and neoplastic colon
 PT cell, useful as vaccine in treating colon cancer and in identifying,
 PT diagnosing, monitoring, staging, imaging colon cancer and non-cancerous
 PT disease state in colon.

XX Claim 1; SEQ ID NO 87; 547P; English.

XX The invention relates to a novel colon specific protein (CSP) (I) and the
 CC nucleic acid (CSNA) encoding it. A CSP of the invention has cytostatic
 CC activity. The protein is useful as a vaccine, and the nucleic acid may
 CC have a use in gene therapy. A CSP is useful for determining the presence
 CC of a colon specific protein in a sample. A CSNA is useful for determining
 CC the presence of a colon specific nucleic acid (CSNA) in a sample. The CSP
 CC and CSNA are useful for diagnosing or monitoring the presence and
 CC metastases of colon cancer in a patient. A method of the invention is
 CC useful for treating a patient with colon cancer. A CSP and CSNA are
 CC useful in identifying, diagnosing, monitoring, staging, imaging colon
 CC cancer and non-cancerous disease state in colon, and as a vaccine for
 CC treating colon cancer and non-cancerous disease states in colon. The
 CC present sequence represents a CSNA of the invention.

XX Sequence 2345 BP; 776 A; 418 C; 625 G; 526 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 2345;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGAGTGTGA 20
 DB 152 ATGATGGCGGCGAGTGTGA 133

RESULT 13

ADRO7433/C

ID ADRO7433 standard; cDNA; 2400 BP.

AC ADRO7433;

DT 04-NOV-2004 (first entry)

DE Full length human cDNA useful for treating neurological disease Seq 939.

XX gene; ss: human; oligo-capping method; diagnostic marker; gene therapy;

XX osteoporosis; neurological disease; Alzheimer's disease;

XX Parkinson's disease; dementia; short memory; cancer;

XX sense or motor function; emotional reaction; fear response; panic;

XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;

XX tranquilizer.

XX Homo sapiens.

XX EP1447413-A2.

XX 18-AUG-2004.

XX 12-FEB-2004; 2004EP-00001145.

XX 14-FEB-2003; 2003JP-00102207.

XX 09-MAY-2003; 2003JP-00131452.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Yamamoto J, Nishikawa T, Igono Y, Sugiyama T, Otsuki T;

XX Wakamatsu A, Ishii S, Nagai K, Irie R;

XX WPI; 2004-583265/57.

XX P-PSDB; ADR09389.

XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,

XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX Claim 1; SEQ ID NO 939; 2686bp; English.

XX This invention relates to novel, isolated full length human cDNA

XX molecules and the encoded proteins thereof. Specifically, it refers to

XX cDNA clones obtained by an oligo-capping method, where none of these

XX clones are identical to any known human mRNAs. The present invention

XX describes an immunosay to identify agonists and antagonists, as well as

XX antibodies, antisense molecules and siRNAs that can all be used to bind

XX to and modulate expression of the cDNA molecules. As such, these

XX molecules are useful for diagnostic markers or therapeutic targets for

XX the various diseases or morbid states. In particular, they are useful in

XX gene therapy for treating osteoporosis, neurological disease, Alzheimer's

XX disease, Parkinson's disease, dementia, short memory and various cancers,

XX as well as for maintaining equilibrium of sense or motor function, and

XX for treating emotional reaction, fear response and panic. Accordingly,

XX they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,

XX cyostatic and tranquilizer activities. This polynucleotide is a full

XX length human cDNA sequence of the invention. NOTE: This sequence is not

XX given in the sequence listing of the specification but can be obtained on

XX CD-ROM from the European Patent Office, Vienna Sub-office.

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RESULT 14

AAV71745/C

ID AAV71745 standard; cDNA; 2518 BP.

AC AAV71745;

DT 15-MAR-1999 (first entry)

DE Human V3 loop HIV receptor P95/nucleolin cDNA.

XX HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;

XX P95 protein; nucleolin; infection; therapy; diagnosis; ss.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX CDS 112..2235

XX /*tag= a

XX WO9840480-A1.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-EP001409.

XX 12-MAR-1997; 97US-0040969P.

XX (INSP) INST PASTEUR.

XX (CNRS) CENT NAT RECH SCI.

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RESULT 15

AAC92553/C

ID AAC92553 standard; DNA; 2518 BP.

AC AAC92553;

DT 15-MAR-1999 (first entry)

DE Human V3 loop HIV receptor P95/nucleolin cDNA.

XX HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;

XX P95 protein; nucleolin; infection; therapy; diagnosis; ss.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX CDS 112..2235

XX /*tag= a

XX WO9840480-A1.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-EP001409.

XX 12-MAR-1997; 97US-0040969P.

XX (INSP) INST PASTEUR.

XX (CNRS) CENT NAT RECH SCI.

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XX AAC92553;

XX 27-MAR-2001 (first entry)

XX Human nucleolin DNA.

XX Human nucleolin; P92; C23; phosphoprotein; ribosome biogenesis;
 KW ribosome transport; cytokinesis; nucleogenesis; cell proliferation;
 KW cell growth; transcriptional repression; replication;
 KW signal transduction; chromatin decondensation; Ag-NOR family;
 KW nucleolin antibody; systemic connective tissue disease; SLR;
 KW systemic lupus erythematosus;
 KW scleroderma-like chronic graft versus host disease;
 KW expression inhibition; antisense therapy; tumour formation; cancer;
 KW inflammation; immune disorder; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 112..2235
 XX /tag= a
 XX /product= "Human nucleolin"

XX US6165786-A.

XX 26-DEC-2000.

XX 03-NOV-1999; 99US-00433699.

XX 03-NOV-1999; 99US-00433699.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowsett LM;

XX WPI; 2001-079848/09.

XX P-PSDB; AAB48964.

XX Novel antisense compound targeted to human nucleolin which specifically
 PT hybridizes with and inhibits the expression of human nucleolin, useful
 PT for modulating the expression of nucleolin in cells.

XX Claim 1; Col 47-52; 41pp; English.

XX This sequence represents DNA encoding human nucleolin. Nucleolin (also
 CC known as P92 or C23) is the most abundant nucleolar phosphoprotein in
 CC actively growing cells. Nucleolin primarily participates in ribosome
 CC biogenesis and transport of ribosomal components, being able to
 CC transiently bind to pre-ribosomes in the nucleolus via a
 CC ribonucleoprotein consensus sequence. However, it has also been shown to
 CC be involved in cytokinesis, nucleogenesis, cell proliferation and growth,
 CC transcriptional repression, replication, signal transduction, and
 CC chromatin decondensation. Nucleolin is a member of the Ag-NOR (active
 CC ribosomal gene located in the nucleolar organizer region) family of
 CC proteins which are markers of active ribosomal genes, and whose
 CC expression is associated with the prediction of tumour growth rate. The
 CC presence of antibodies against nucleolin are associated with systemic
 CC connective tissue diseases such as systemic lupus erythematosus (SLE) and
 CC scleroderma-like chronic graft versus host disease. The invention relates
 CC to antisense oligonucleotides targeted to the nucleolin gene, which
 CC inhibit its expression. A series of oligonucleotides (AAC92560-C92639)
 CC were designed to target different regions of the human nucleolin mRNA,
 CC and were analysed for their effect on nucleolin mRNA levels by
 CC quantitative real-time PCR. The oligonucleotides of the invention are
 CC useful for diagnosis, prevention and treatment of conditions associated
 CC with nucleolin expression, such as tumour formation, immune disorders and
 CC inflammation

XX Sequence 2518 BP; 823 A; 459 C; 711 G; 525 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 100.0%; Score 20; DB 4; Length 2518;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATCGCGCGGAGTGTGA 20

Db 113 ATGATCGCGCGGAGTGTGA 94

Search completed: April 11, 2005, 23:56:49
 Job time : 432 secs